

1 CCCACGCGTCCGGTCGGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA
 61 GCTCAAAGGGCCCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT
 121 CCAGAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG
 181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC
 241 TGAGAGAGTTCTGGGTGTCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
 301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTG
 361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA
 421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGC
 481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT
 541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTC
 601 TCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
 661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG
 721 AAAGCAGAGGAACTGCTGTTGTTACCTGGGAACCCTGGAGGGGCCTTCCTCATCCGGGAG
 781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTCTGAGTCCGCCTCAGCCGCCCTGCATCCTGG
 841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG
 901 CGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGAC
 961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTGCAGAGGGCTGGCCCGCTCCCTGGCAAG
 1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC
 1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
 1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
 1201 GCCCAAAGGAGAGGCCAAAAGGGAAACCAAGGCTGCACACCTAGAACCCCAATTACGCCT
 1261 CCTGGGCACCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC
 1321 ATCTAGGGTCCCACCTGTACCCTTGCTCTTTCTCTCTTAGCCCTTAGAAGTCACCTACT
 1381 TCCTTCCAGTGCCATGATCCACCTGCGACCTCTAGTGCGAGTGCAGAGAAGGTGGGACC
 1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG
 1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
 1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
 1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACTCAGAAGGTAGGACTGT
 1681 GGCCTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGG
 1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCCTCAA
 1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTGGAGACGGAGTCTT
 1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCAGCATCTCAGCTCACTGCAACCTCCATCTC
 1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
 1981 CACCATGCCTGGCTAATTTTTTTGTATTTTTTAGTAGACATGGGGTTTCACCACATTGGCC
 2041 AGGCTGGTGTGGAACCTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG
 2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTTCAATTTGTG
 2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
 2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
 2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC
 2341 CCTTGATTTCCCTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
 2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTC
 2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTCTCAATTAA
 2521 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAA

FIG. 1



1 CCCACGCGTCCGGTCCGGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA
61 GCTCAAAGGGCCCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT
121 CCAGAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG
181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC
241 TGAGAGAGTTCTGGGTGTCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTG
361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA
1 M G
421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGC
3 S L P S R R K S L P S P S L S S S V Q G
481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT
23 Q G P V T M E A E R S K A T A V A L G S
541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTC
43 F P A G G P A E L S L R L G E P L T I V
601 TCTGAGGATGGAGACTGGTGGACGGTGTCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
63 S E D G D W W T V L S E V S G R E Y N I
661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG
83 P S V H V A K V S H G W L Y E G L S R E
721 AAAGCAGAGGAACTGCTGTTGTTACCTGGGAACCCTGGAGGGGCCTTCCTCATCCGGGAG
103 K A E E L L L L P G N P G G A F L I R E
781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTCTCAGTCCGCCTCAGCCGCCCTGCATCCTGG
123 S Q T R R G S Y S L S V R L S R P A S W
841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG
143 D R I R H Y R I H C L D N G W L Y I S P
901 CGCCTCACCTTCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGAC
163 R L T F P S L Q A L V D H Y S E L A D D
961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTCTGAGAGGGCTGGCCCGCTCCCTGGCAAG
183 I C C L L K E P C V L Q R A G P L P G K
1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC
203 D I P L P V T V Q R T P L N W K E L D S
1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
223 S L L F S E A A T G E E S L L S E G L R
1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
243 E S L S F Y I S L N D E A V S L D D A *
1201 GCCCAAAGGAGAGGCCAAAAGGGAAACCAAGGCTGCACACCTAGAACCCCAATTACGCCT
1261 CCTGGGCACCCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC
1321 ATCTAGGGTCCCACCTGTACCCTTGCTCTTTCCTCTCTTAGCCCTTAGAAGTCACCTACT
1381 TCCTTCCAGTGCCATGATCCCACCTGCGACCTCTAGTGCGAGTGCAGAGAAGGTGGGACC
1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG
1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT

FIG. 3A



1681 GGCCTAGAAGGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGG
1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCCTCAA
1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTTTGAGACGGAGTCTT
1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC
1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
1981 CACCATGCCTGGCTAATTTTTTTGTATTTTGTAGTAGACATGGGGTTTCACCACATTGGCC
2041 AGGCTGGTGTGCGAACTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG
2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTTCAATTTTGTG
2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC
2341 CCTTGATTTCCTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTC
2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA
2522 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAA

FIG.3B

Homology	Amino acid level	
	Similarity	Identity
human SLAP x mouse SLAP	89.9%	88.0%
human SLAP x human SLAP-2	58.4%	47.4%
mouse SLAP x human SLAP-2	70.0%	58.1%

FIG. 4

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hSLAP-2      1 MGS LPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAE
               : . || |. | . : | . | : | .
hSLAP        1 ...MGNSMKSTPAPA.....ERLPNPEGLDSDFLAVLSDYPSPDISP

51 LSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLS
   | || | :| :| :| || :| .|| | | : || :| ||| :|||
41 PIFRRGEKLRVISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLG

101 REKAEELLLLPGNPGGAF LIRESQTRRGSYSLSVRLSRPASWDRI RHYRI
   |:||||| || |. |:||||| :| :| ||||| .: :|||
91 RDKAEELLQLPDTKVG SFMIRESETKKGFYSLSVR.....HRQVKHYRI

151 HCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCVLQ RAGPLP
   | | | ||||| | : ||. ||||. || :||. | ||. |
135 FRLPNNWYYISPRLTFQCLEDLVNHYSEVADGLCCVLTTPCLTQSTAAPA

201 GKDIPLPVTVQRTPLNWK...ELDSSLLFSEAATG.EESLLSEGLRESLS
   : |||... ..| : | | :||| | |||| :.
185 VRASSSPVTLRQKTVDWRRVSRLQEDPEGTENPLGVDES LFSYGLRESIA

247 FYISLNDEAVSLDDA.....
   |:|| | . |
235 SYLSLTSEDNTSFDRKKKSISLMYGGSKRKSSFFSSPPYFED

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FIG. 5



hSLAP 1 MGNSMKSTPAPAERPLPNPEGLDSDFLAVLSDYPSPDISPPIFRRGEKLR
||||||| |.|||| |. |||:|||||||.|||||||
mSLAP 1 MGNSMKSTSPPSERPLSSSEGLESDFLAVLTDYPSPDISPPIFRRGEKLR

51 VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL
|||||||
51 VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL

101 PDKVGSFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF
||||:|||||||
101 PDKIGSFMIRESSETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF

151 QCLEDLVNHYSEVADGLCCVLTTPCLTQSTAAPAVRAS.....SSPVTLR
||||| ||||| ||||| |. || | |||||
151 QCLEDLVTHYSEVADGLCCVLTTPCLAQNI PAPTSHPS PCTSPGSPVTLR

196 QKTVDWRRVSRLQEDPEGTENPLGVDESLSYGLRESIASYLSLTSEDNT
||| ||:||||| || |||| ||||| ||||| :|..
201 QKTFDWKRVSRLQEGSEGAENPLRVDESLSYGLRESIASYLSLTGDDSS

246 SFDRKKKSISL MYGGSKRKSSFFSPPYFED 276
|||||||:|||| ||||| |||||
251 SFDRKKKSLSL MYTGSKRKSSFFSAPQYFED 281

FIG. 6

hSLAP-2

mSLAP

1 MG.SLPSRRKSLPS..PSLSSSVQGQGPVTMEAERSKATAVALGSFPAGG
|| |: | | | | | | | | :| :| | | | :|. |
1 MGNSMKS..TSPPSERP.LSSS...EG...LE...SDFLAV.LTDYPS..

48 PAELS...LRLGEPLTIVSEDGDWWTVLSEVS.GRE.YNIPSVHVAKVSH
| :| | | | | | | | | :| :| | | | | | : | | :| | |
36 P.DISPPIFRRGEKLRVISDEGGWWKAIS.LSTGRESY.IPGICVARVYH

93 GWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASW
| | :| | | | | | | | | | | | | | | | | | | | | | | | | |
83 GWLFEGGLGRDKAEELLQLPDTKIGSFMIRESETKKGFYSLSVR.HR....

143 DRIRHYRIHCLDNGWLYISPRLTFFPSLQALVDHYSELADDICCLLKEPCV
.: :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
128 .QVKHYRIFRLPNNWYYISPRLTFFQCLEDLVTHYSEVADGLCCVLTTPCL

193 LQR..A.....GPL..PGKDIPLPVTV.QRTPLNWKELDSSLLFSEAATG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
177 AQNIPAPTSHPSPTSPGS....PVTLRQKT.FDWKRV.SRL..QEGSEG

233 .E.....ESLLSEGLRESLSFYISL.NDEAVSLD
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
219 AENPLRVDESLSFYGLRESIASYLSLTGDDSSSFD

FIG. 7

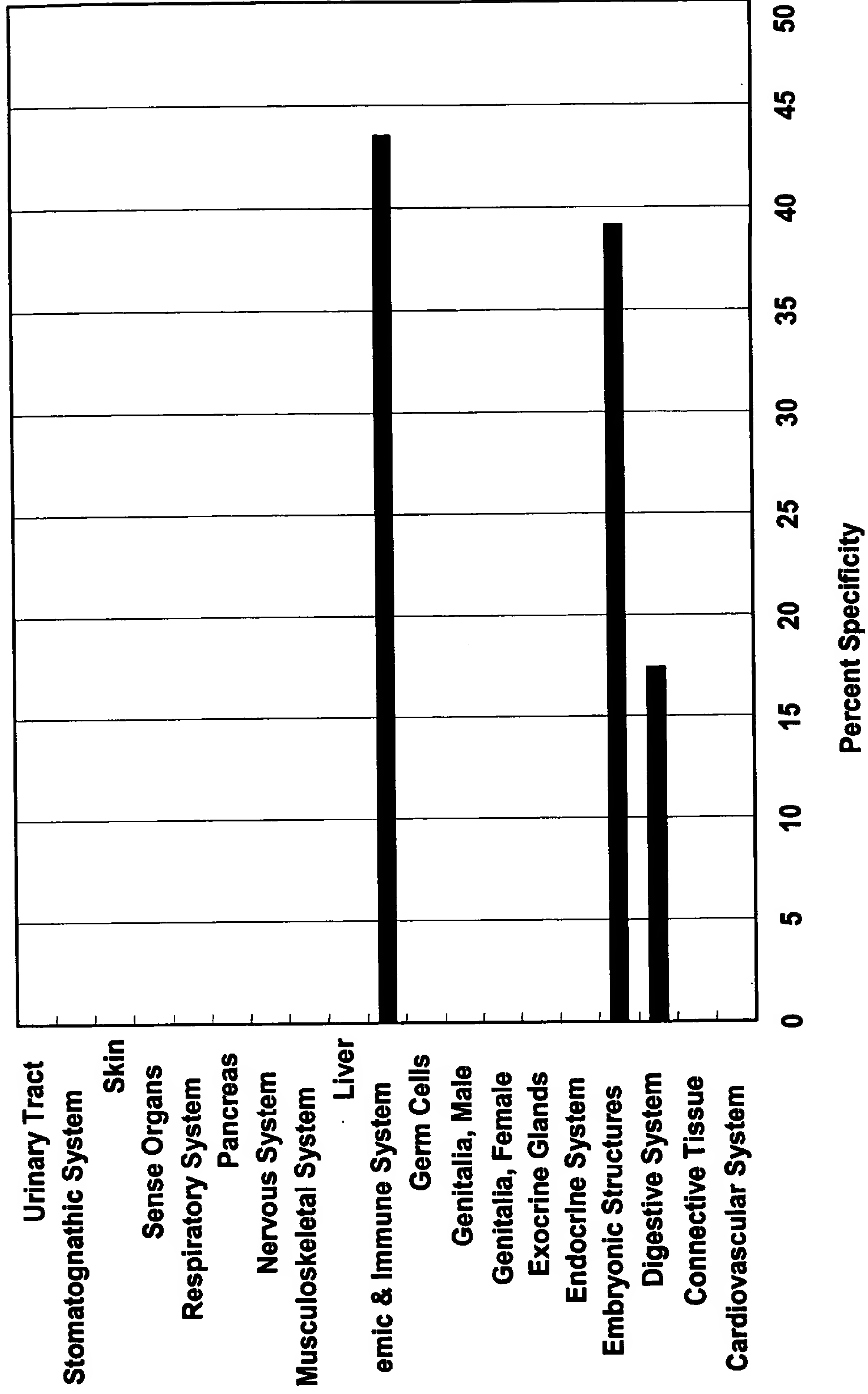


FIG. 8